

Attack.
paper
#10



RESULTS OF BLAST

BLASTP 2.2.1 [Apr-13-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1006356104-14842-14592

Query=

(131 letters)

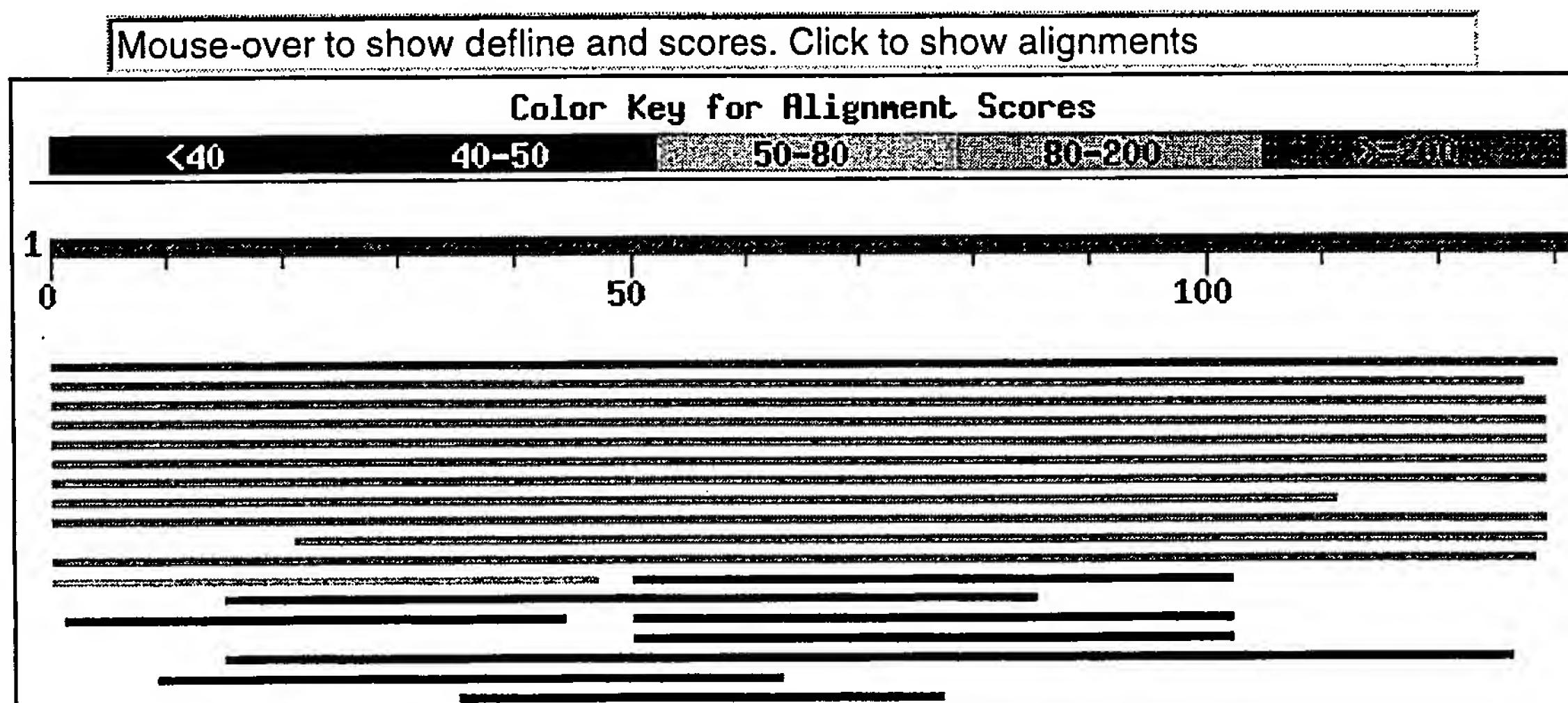
Database: nr

799,241 sequences; 254,026,857 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 20 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Score (bits)	E Value
-----------------	------------

gi 7528274 gb AAF63204.1 AF244915_1	(AF244915)	interleukin-...	244	1e-64
gi 14573528 gb AAK68108.1 AF385625_1	(AF385625)	interleukin...	179	4e-45
gi 2905620 gb AAC03535.1	(AF043334)	interleukin 13 precurs...	169	4e-42
gi 4504645 ref NP_002179.1	(NM_002188)	interleukin 13 [Hom...	169	5e-42
gi 2144691 pir A47481	interleukin-13 precursor - human >gi...		167	1e-41

gi 7387804 sp Q9XSV9 IL13_BOVIN	INTERLEUKIN-13 PRECURSOR (1...	161	8e-40
gi 1127548 gb AAA83738.1	(U10307) interleukin 13 [Homo sap...	160	1e-39
gi 4558814 gb AAD22748.1 AF072807_1	(AF072807) interleukin-...	146	3e-35
gi 6680403 ref NP_032381.1	(NM_008355) interleukin 13 [Mus...	143	3e-34
gi 14719448 pdb 1GA3 A	Chain A, Nmr Structure Of Interleuki...	141	1e-33
gi 16758680 ref NP_446280.1	(NM_053828) interleukin 13 [Ra...	139	4e-33
gi 258577 gb AAB23881.1	P600 homolog [human, Peptide, 49 aa]	61	1e-09
gi 451840 gb AAA61629.1	(U05203) putative preprosperminoge...	31	1.8
gi 16760873 ref NP_456490.1	(NC_003198) flagellar transcri...	31	1.8
gi 7387658 sp O52222 FLHC_SALTY	FLAGELLAR TRANSCRIPTIONAL A...	30	2.8
gi 16765266 ref NP_460881.1	(NC_003197) regulator of flage...	30	2.9
gi 14485571 gb AAK63010.1 AF320026_1	(AF320026) heme oxygen...	30	3.6
gi 11466430 ref NP_038436.1	(NC_002186) putative plastid d...	30	4.4
gi 1293576 gb AAA98646.1	(U49765) immunoglobulin heavy cha...	30	5.4
gi 15641617 ref NP_231249.1	(NC_002505) conserved hypothet...	29	8.0

Alignments

>gi|7528274|gb|AAF63204.1|AF244915_1 (AF244915) interleukin-13 [Canis familiaris]
Length = 131

Score = 244 bits (622), Expect = 1e-64
Identities = 131/131 (100%), Positives = 131/131 (100%)

Query: 1 MALWLTVVIALTCLGGLASPSPVTPSPTLKELIEELVNITQNQASLCNGSMVWSVNLTAG 60

MALWLTVVIALTCLGGLASPSPVTPSPTLKELIEELVNITQNQASLCNGSMVWSVNLTAG

Sbjct: 1 MALWLTVVIALTCLGGLASPSPVTPSPTLKELIEELVNITQNQASLCNGSMVWSVNLTAG 60

Query: 61 MYCAALESLINVSDCSAIQRTQRMLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTY 120

MYCAALESLINVSDCSAIQRTQRMLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTY

Sbjct: 61 MYCAALESLINVSDCSAIQRTQRMLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTY 120

Query: 121 VRGVYRHGNFR 131

VRGVYRHGNFR

Sbjct: 121 VRGVYRHGNFR 131

>gi|14573528|gb|AAK68108.1|AF385625_1 (AF385625) interleukin-13 [Sus scrofa]

gi|14594692|gb|AAK68109.2|AF385626_1 (AF385626) interleukin-13 [Sus scrofa]

Length = 131

Score = 179 bits (454), Expect = 4e-45

Identities = 96/131 (73%), Positives = 108/131 (82%), Gaps = 3/131 (2%)

Query: 1 MALWLTVVIALTCLGGLASPSPVTPSPT-LKELIEELVNITQNQAS-LCNGSMVWSVNLT 58

MALWLT+VIALTC GGLASP PV P T LKELIEELVNITQNQ + LCNGSMVWSVNLT

Sbjct: 1 MALWLTLVIALTCFGGLASPGPVPPHSTALKELIEELVNITQNQKTPLCNGSMVWSVNLT 60

Query: 59 AGM-YCAALESLINVSDCSAIQRTQRMLKALCSQKPAAGQISSERSRDTKIEVIQLVKNL 117

M YCAALESLIN+SDCSAIQ+TQRML ALCS KP + Q+ + RDTKIEV Q VK+L

Sbjct: 61 TSMQYCAALESLINISDCSAIQKTQRMLSALCSHKPPSEQVPGKHIRDtkievaqfvkdl 120

Query: 118 LTYVRGVYRHG 128

L ++R ++RHG

Sbjct: 121 LKHLRMIFRHG 131

>gi|2905620|gb|AAC03535.1| (AF043334) interleukin 13 precursor [Homo sapiens]

Length = 132

Score = 169 bits (428), Expect = 4e-42
 Identities = 94/131 (71%), Positives = 105/131 (79%), Gaps = 1/131 (0%)

Query: 1 MALWLTVVIALTCLGGLASPSPVTPSPTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTA 59
 MAL LT VIALTCLGG ASP PV PS L+ELIEELVNITQNQ A LCNGSMVWS+NLTA

Sbjct: 1 MALLLTTVIALTCLGGFASPGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTA 60

Query: 60 GMYCAALESLINVSDCSAIQRTQRMLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119
 GMYCAALESLINVS CSAI++TQRML C K +AGQ SS RDTKIEV Q VK+LL

Sbjct: 61 GMYCAALESLINVSGCSAIEKTQRMLGGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLL 120

Query: 120 YVRGVYRHGNF 130

+++ ++R G F

Sbjct: 121 HLKKLFREGRF 131

* >gi|4504645|ref|NP_002179.1| (NM_002188) interleukin 13 [Homo sapiens]
 gi|15297318|ref|XP_054534.1| (XM_054534) interleukin 13 [Homo sapiens]
 gi|15297320|ref|XP_054533.1| (XM_054533) hypothetical protein XP_054533 [Homo sapiens]
 gi|16171723|ref|XP_055221.1| (XM_055221) hypothetical protein XP_055221 [Homo sapiens]
 gi|462408|sp|P35225|IL13_HUMAN INTERLEUKIN-13 PRECURSOR (IL-13)
 gi|186276|gb|AAA36107.1| (L06801) interleukin 13 [Homo sapiens]
 gi|673420|emb|CAA48824.1| (X69079) alternative; ATG at 15 is an alternative start codon [Homo sapiens]
 gi|1045452|gb|AAB01681.1| (U31120) interleukin-13 precursor [Homo sapiens]
 gi|14091716|gb|AAK53823.1|AF377331_1 (AF377331) interleukin 13 [Homo sapiens]

Length = 132

Score = 169 bits (427), Expect = 5e-42
 Identities = 94/131 (71%), Positives = 105/131 (79%), Gaps = 1/131 (0%)

Query: 1 MALWLTVVIALTCLGGLASPSPVTPSPTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTA 59
 MAL LT VIALTCLGG ASP PV PS L+ELIEELVNITQNQ A LCNGSMVWS+NLTA

Sbjct: 1 MALLLTTVIALTCLGGFASPGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTA 60

Query: 60 GMYCAALESLINVSDCSAIQRTQRMLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119
 GMYCAALESLINVS CSAI++TQRML C K +AGQ SS RDTKIEV Q VK+LL

Sbjct: 61 GMYCAALESLINVSGCSAIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLL 120

Query: 120 YVRGVYRHGNF 130

+++ ++R G F

Sbjct: 121 HLKKLFREGRF 131

>gi|2144691|pir||A47481 interleukin-13 precursor - human
 gi|580330|emb|CAA48823.1| (X69079) alternative; ATG at 15 is an alternative start codon [Homo sapiens]
 gi|445575|prf||1909326A interleukin 13 [Homo sapiens]

Length = 146

Score = 167 bits (424), Expect = 1e-41
 Identities = 94/131 (71%), Positives = 105/131 (79%), Gaps = 1/131 (0%)

Query: 1 MALWLTVVIALTCLGGLASPSPVTPSPTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTA 59

MAL LT VIALTCLGG ASP PV PS L+ELIEELVNITQNQ A LCNGSMVWS+NLTA

Sbjct: 15 MALLLTTVIALTCLGGFASPGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTA 74

Query: 60 GMYCAALESLINVSDCSAIQRTQRMLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119
 GMYCAALESLINVS CSAI++TQRML C K +AGQ SS RDTKIEV Q VK+LL
 Sbjct: 75 GMYCAALESLINVSGCSAIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLL 134

Query: 120 YVRGVYRHGNF 130
 +++ ++R G F
 Sbjct: 135 HLKKLFREGRF 145

>gi|7387804|sp|Q9XSV9|IL13_BOVIN INTERLEUKIN-13 PRECURSOR (IL-13)
gi|5420145|emb|CAB46636.1| (AJ132441) interleukin-13 [Bos taurus]
 Length = 132

Score = 161 bits (408), Expect = 8e-40
 Identities = 87/131 (66%), Positives = 103/131 (78%), Gaps = 1/131 (0%)

Query: 1 MALWLTVVIALTCLGGLASPSPVTPSPTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTA 59
 MAL LT VI L C GGL SPSPV + LKELIEELVNITQNQ LCNGSMVWS+NLT+
 Sbjct: 1 MALLTAVIVLICFGGLTSPSPVPSATALKELIEELVNITQNQVPLCNGSMVWSLN LTS 60

Query: 60 GMYCAALESLINVSDCSAIQRTQRMLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119
 MYCAAL+SLI++S+CS IQRT++ML ALC KP+A Q+SSE RDTKIEV Q +K+LL
 Sbjct: 61 SMYCAALDSLISISNCVSIQRTKKMLNALCPHKPSAKQVSSEYVRDTKIEVAQFLKDLLR 120

Query: 120 YVRGVYRHGNF 130
 + R V+R+ F
 Sbjct: 121 HSРИVFRNERF 131

>gi|1127548|gb|AAA83738.1| (U10307) interleukin 13 [Homo sapiens]
 Length = 131

Score = 160 bits (406), Expect = 1e-39
 Identities = 92/131 (70%), Positives = 103/131 (78%), Gaps = 2/131 (1%)

Query: 1 MALWLTVVIALTCLGGLASPSPVTPSPTLKELIEELVNITQNQAS-LCNGSMVWSVNLTA 59
 MAL LT VIALTCLGG ASP PV PS L+ELIEELVNITQNQ LCNGSMVWS+NLT+
 Sbjct: 1 MALLTTVIALTCLGGFASPGPVPPSTALRELIEELVNITQNQKRPLCNGSMVWSINLTA 60

Query: 60 GMYCAALESLINVSDCSAIQRTQRMLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119
 GMYCAALESLINVS CSAI++TQRML C K +AG SS RDTKIEV Q VK+LL
 Sbjct: 61 GMYCAALESLINVSGCSAIEKTQRMLSGFCPHKVSAG-FSSLHVRDTKIEVAQFVKDLLL 119

Query: 120 YVRGVYRHGNF 130
 +++ ++R G F
 Sbjct: 120 HLKKLFREGRF 130

>gi|4558814|gb|AAD22748.1|AF072807_1 (AF072807) interleukin-13 precursor [Bos taurus]
 Length = 114

Score = 146 bits (368), Expect = 3e-35
 Identities = 81/113 (71%), Positives = 91/113 (79%), Gaps = 1/113 (0%)

Query: 1 MALWLTVVIALTCLGGLASPSPVTPSPTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTA 59
 MAL LT VI L C GGL SPSPV + LKELIEELVNITQNQ LCNGSMVWS+NLT+

Sbjct: 1 MALLTAVIVLICFGGLTSPSPVPSATALKELIEELVNITQNQKVPLCNGSMVWSLNLT 60
 Query: 60 GMYCAALESLINVSDCSAIQRTQRMLKALCSQKPAAGQISSERSRDTKIEVIQ 112
 MYCAAL+SLI++S+CS IQRT+RML ALC KP+A Q+SSE RDTKIEV Q
 Sbjct: 61 SMYCAALDSLISISNCNSVIQRTKRMLNALCPHKPSAKQVSSEYVRDTKIEVAQ 113

>gi|6680403|ref|NP_032381.1| (NM_008355) interleukin 13 [Mus musculus]
 gi|129377|sp|P20109|IL13_MOUSE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION
 gi|91336|pir||E30552 T-cell activation protein P600 precursor - mouse
 gi|533247|gb|AAA40149.1| (M23504) T cell secreted protein [Mus musculus]
 Length = 131

Score = 143 bits (360), Expect = 3e-34
 Identities = 79/134 (58%), Positives = 98/134 (72%), Gaps = 7/134 (5%)

Query: 1 MALWLTVVIALTCLGGLASPSPVTPSP----TLKELIEELVNITQNQASLCNGSMVWSVN 56
 MALW+T V+AL CLGGLA+P PV S TLKELIEEL NITQ+Q LCNGSMVWSV+
 Sbjct: 1 MALWVTAVLALACLGGLAAPGPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVD 60

Query: 57 LTAGMYCAALESLINVSDCSAIQRTQRMLKALCSQKPAAGQISSERSRDTKIEVIQLVKN 116
 L AG +C AL+SL N+S+C+AI RTQR+L LC++K A +SS DTKIEV +
 Sbjct: 61 LAAGGFVALIDSLTNISNCNAIYRTQRILHGLCNRK-APTTVSS--LPDTKIEVAHFITK 117

Query: 117 LLTYVRGVYRHGNF 130
 LL+Y + ++RHG F
 Sbjct: 118 LLSYTKQLFRHGPF 131

>gi|14719448|pdb|1GA3|A Chain A, Nmr Structure Of Interleukin-13
 Length = 113

Score = 141 bits (355), Expect = 1e-33
 Identities = 77/110 (70%), Positives = 88/110 (80%), Gaps = 1/110 (0%)

Query: 22 PVTPSPTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAIQR 80
 PV PS L+ELIEELVNITQNQ A LCNGSMVWS+NLTAGMYCAALESLINVS CSAI++
 Sbjct: 3 PVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEK 62

Query: 81 TQRMLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 130
 TQRML C K +AGQ SS RDTKIEV Q VK+LL +++ ++R G F
 Sbjct: 63 TQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKKLFREGRF 112

>gi|16758680|ref|NP_446280.1| (NM_053828) interleukin 13 [Rattus norvegicus]
 gi|1170528|sp|P42203|IL13_RAT INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION P
 gi|2118664|pir||I52290 interleukin-13 - rat
 gi|438876|gb|AAA16478.1| (L26913) interleukin-13 [Rattus norvegicus]
 Length = 131

Score = 139 bits (350), Expect = 4e-33
 Identities = 79/134 (58%), Positives = 99/134 (72%), Gaps = 8/134 (5%)

Query: 1 MALWLTVVIALTCLGGLASPSPV----TPSPTLKELIEELVNITQNQ-ASLCNGSMVWSV 55
 MALW+T V+AL CLGGLA+P PV +P L+ELIEEL NITQ+Q SLCN SMVWSV
 Sbjct: 1 MALWVTAVLALACLGGLATPGPVRRSTSPPVALRELIEELSNITQDQKTSLCNSSMVWSV 60

Query: 56 NLTAGMYCAALESLINVSDCSAIQRTQRMLKALCSQKPAAGQISSERSRDTKIEVIQLVK 115
 +LTAG +CAALES N+S C+AI RTQR+L LC+QK A ++S DTKIEV Q +
 Sbjct: 61 DLTAGGFCAALESLTNISSCNAIHTQRILNGLCNQK--ASDVASS-PPDTKIEVAQFIS 117
 LL Y + ++R+G+
 Sbjct: 118 KLLNYSKQLFRYGH 131

>gi|258577|gb|AAB23881.1| P600 homolog [human, Peptide, 49 aa]
 Length = 49

Score = 61.2 bits (147), Expect = 1e-09
 Identities = 35/49 (71%), Positives = 36/49 (73%), Gaps = 1/49 (2%)

Query: 1 MALWLTVVIALTCLGGLASPSPVTPSPTLKELIEELVNITQNQ-ASLCN 48
 MAL LT VIAL CLGG SP PV PS L+ELIEL NITQ Q A LCN
 Sbjct: 1 MALLLTTVIALACLGGFDSPGPVPPSTALRELIEELSNITQTQKAPLCN 49

>gi|451840|gb|AAA61629.1| (U05203) putative preprosperminogen [Oryctolagus cuniculus
 Length = 275

Score = 31.2 bits (69), Expect = 1.8
 Identities = 21/71 (29%), Positives = 33/71 (45%), Gaps = 6/71 (8%)

Query: 16 GLASPSPVTPSPTLKELIEELVNITQNQASLCNGSMVWSVNLTAGMYCAALESLINVSDC 75
 G + PSPTL E +L+N+ LCN + ++ +TA CA S + C
 Sbjct: 181 GYVKENAPRPSPTLMEARVDLINL-----ELCNSTQWYNGRITASNLCAGYPMSG-KIDTC 234

Query: 76 SAIQRTQRMLK 86
 +Q+ +LK
 Sbjct: 235 QRLQQQLVEVLK 245

>gi|16760873|ref|NP_456490.1| (NC_003198) flagellar transcriptional activator [Salmo
 enterica subsp. enterica serovar Typhi]
gi|16503170|emb|CAD05675.1| (AL627272) flagellar transcriptional activator [Salmone
 subsp. enterica serovar Typhi]
 Length = 194

Score = 31.2 bits (69), Expect = 1.8
 Identities = 16/56 (28%), Positives = 26/56 (45%), Gaps = 3/56 (5%)

Query: 51 MVWSVNLTAGMYCAALESLINVSDCS---AIQRTQRMLKALCSQKPAAGQISSERS 103
 M W N+ A M+C A + L+ CS A+ + R+ C Q P ++ R+
 Sbjct: 67 MTWEQNIHASMFCNAWQFLLKTGLCSGVDAVIKAYRLYLEQCPQPPEGSLLALTRA 122

>gi|7387658|sp|052222|FLHC_SALTY FLAGELLAR TRANSCRIPTIONAL ACTIVATOR FLHC
gi|2772918|gb|AAB96640.1| (AF029300) FlhC [Salmonella typhimurium]
gi|6045176|dbj|BAA85315.1| (D43640) FlhC protein [Salmonella typhimurium]
 Length = 192

Score = 30.4 bits (67), Expect = 2.8
 Identities = 16/56 (28%), Positives = 26/56 (45%), Gaps = 3/56 (5%)

Sbjct: 44 ALECLGGVSGGGITDYNPALRSRLTIMKDDSKNQVSLSSLSSV--TLEDATYYCA 96

>gi|15641617|ref|NP_231249.1| (NC_002505) conserved hypothetical protein [Vibrio cho
 gi|11354623|pir||C82178 conserved hypothetical protein VC1609 [imported] - Vibrio
 cholerae (group O1 strain N16961)
 gi|9656121|gb|AAF94763.1| (AE004238) conserved hypothetical protein [Vibrio cholera
 Length = 408

Score = 28.9 bits (63), Expect = 8.0
 Identities = 18/48 (37%), Positives = 27/48 (55%), Gaps = 4/48 (8%)

Query: 2 ALWLTVVIALTCLGGLASPSPVTPSPTLKELIEE----LVNITQNQAS 45
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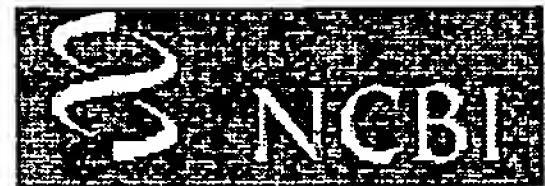
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 Posted date: Nov 16, 2001 11:40 PM
 Number of letters in database: 254,026,857
 Number of sequences in database: 799,241

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Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
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 Number of Sequences: 799241
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 Number of successful extensions: 5801
 Number of sequences better than 10.0: 32
 Number of HSP's better than 10.0 without gapping: 17
 Number of HSP's successfully gapped in prelim test: 15
 Number of HSP's that attempted gapping in prelim test: 5767
 Number of HSP's gapped (non-prelim): 32
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 effective HSP length: 107
 effective length of query: 24
 effective length of database: 168,508,070
 effective search space: 4044193680
 effective search space used: 4044193680
 T: 11
 A: 40
 X1: 16 (7.4 bits)
 X2: 38 (14.6 bits)
 X3: 64 (24.7 bits)
 S1: 41 (21.8 bits)
 S2: 63 (28.9 bits)



PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM Book

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1: P35225. INTERLEUKIN-13 PR...

BLink, Related Sequences, OMIM, PubMed, Taxonomy,

[gi:462408]

LinkOut

LOCUS	IL13_HUMAN	132 aa	PRI	20-AUG-2001
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PID	g462408			
VERSION	P35225 GI:462408			
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KEYWORDS	Cytokine; Glycoprotein; Signal; 3D-structure; Polymorphism.			
SOURCE	human.			
ORGANISM	<u>Homo sapiens</u> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (residues 1 to 132)			
AUTHORS	Minty,A.J., Chalon,P., Derocq,J.M., Dumont,X., Guillemot,J.C., Kaghad,M., Labit,C., Leplatois,P., Liauzun,P., Miloux,B., Minty,C., Casellas,P., Loison,G., Lupker,J., Shire,D., Ferrara,P. and Caput,D.			
TITLE	Interleukin-13 is a new human lymphokine regulating inflammatory and immune responses			
JOURNAL	Nature 362 (6417), 248-250 (1993)			
MEDLINE	<u>93211479</u>			
REMARK	SEQUENCE FROM N.A.			
REFERENCE	2 (residues 1 to 132)			
AUTHORS	McKenzie,A.N., Culpepper,J.A., Waal Malefyt,R., Briere,F., Punnonen,J., Aversa,G., Sato,A., Dang,W., Cocks,B.G., Menon,S., de Vries,J.E., Banchereau,J. and Zurawski,G.R.			
TITLE	Interleukin 13, a T-cell-derived cytokine that regulates human monocyte and B-cell function			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90 (8), 3735-3739 (1993)			
MEDLINE	<u>93234572</u>			
REMARK	SEQUENCE FROM N.A.			
REFERENCE	3 (residues 1 to 132)			
AUTHORS	Dolganov,G., Lewis,D.B., Lovett,M., Burr,J., Bort,S., Short,D., McGurn,M. and Gibson,C.			
TITLE	Direct Submission			
JOURNAL	Submitted (??-JUL-1995)			
REMARK	SEQUENCE FROM N.A.			

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Region 98
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Region 130
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/note="R -> Q. /FTId=VAR_010037."

ORIGIN
1 mallttvia ltclggfasp gpvppstalr elieelvnit qnqkaplcng smvwsinlta
61 gmycaalesl invsgcsaie ktqrmlsgfc phkvsaggfs slhvrdrtkie vaqfvkdlll
121 hlkklfregr fn
//

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